

PR00907: THRGBOMODULN

Thrombomodulin signature

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Prints Database 35 in Blocks Format, Jul 2002
Made available by the Fred Hutchinson Cancer Research Center
1100 Fairview AV N, A1-162, PO Box 19024, Seattle, WA 98109-1024
Based on PRINTS Database as described by TK Attwood, et al (1994),
NAR 22(17):3590-3596. ID is from PRINTS gc line, AC is from
PRINTS gx line, DE is from PRINTS gt line, BL is BLOCK information.
Each PRINTS motif is represented by one block. For each segment, the
sequence ID is followed by the position of the first residue in the
segment. Sequence weights are shown to the right of each segment. The
higher the weight (maximum 100) the more dissimilar the segment is from
other segments in the block. These weights were obtained using the
position-based method of S Henikoff & JG Henikoff (1994), JMB 243:574-578.

Calibrated with position-specific scoring matrices made with pseudo-counts,
JG Henikoff & S Henikoff (1996), CABIOS 12(2):135-143.

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Block PR00907A

```
ID  THRMBOMODULN; BLOCK
AC  PR00907A; distance from previous block=(232,233)
DE  Thrombomodulin signature
BL  adapted; width=20; seqs=3; 99.5%=823; strength=1362
O35370      ( 232) GHWTREVTGAWNCSVENGGC 100
TRBM MOUSE|P15306 ( 232) GHWAVEATGAWNCSVENGGC 96
TRBM HUMAN|P07204 ( 233) GHWAREAPGAWDCSVENGGC 100
//
```

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Block PR00907B

```
ID  THRMBOMODULN; BLOCK
AC  PR00907B; distance from previous block=(-1,0)
DE  Thrombomodulin signature
BL  adapted; width=17; seqs=3; 99.5%=734; strength=1262
O35370      ( 251) CEYMCNRSANGPRCVCP 84
TRBM MOUSE|P15306 ( 251) CEYLCNRSTNEPRCLCP 84
TRBM HUMAN|P07204 ( 252) CEHACNAIPGAPRCQCP 100
//
```

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Block PR00907C

```
ID  THRMBOMODULN; BLOCK
AC  PR00907C; distance from previous block=(4,4)
DE  Thrombomodulin signature
BL  adapted; width=24; seqs=3; 99.5%=941; strength=1371
O35370      ( 272) LQADGRSCAKPVAQLCNELCQHFC 94
TRBM MOUSE|P15306 ( 272) LQADGRSCARPVVQSCNELCEHFC 88
TRBM HUMAN|P07204 ( 273) LQADGRSCTASATQSCNDLCEHFC 100
//
```

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Block PR00907D

```
ID  THRMBOMODULN; BLOCK
AC  PR00907D; distance from previous block=(48,48)
DE  Thrombomodulin signature
BL  adapted; width=26; seqs=3; 99.5%=994; strength=1481
O35370      ( 344) GGFECRCYDGYELVDGECVEQLDPCF 89
TRBM MOUSE|P15306 ( 344) GGFECFCYDGYELVDGECVELLDPCF 89
TRBM HUMAN|P07204 ( 345) GGFECCHCYPNYDLVDGECVEPVDPCF 100
//
```

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Block PR00907E

```

ID    THRMBOMODULN; BLOCK
AC    PR00907E; distance from previous block=(3,3)
DE    Thrombomodulin signature
BL    adapted; width=23; seqs=3; 99.5%=919; strength=1375
O35370      ( 373) CEYQCQPVNSTHYNCICAEGFAP 91
TRBM MOUSE|P15306 ( 373) CEFQCQPVSPSTDYRCICAPGFAP 100
TRBM HUMAN|P07204 ( 374) CEYQCQPLNQTSYLCVCAEGFAP 97
//

```

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Block PR00907F

```

ID    THRMBOMODULN; BLOCK
AC    PR00907F; distance from previous block=(4,4)
DE    Thrombomodulin signature
BL    adapted; width=19; seqs=3; 99.5%=782; strength=1396
O35370      ( 400) PDRCEMFCNETSCPADCDP 93
TRBM MOUSE|P15306 ( 400) PHKCEMFCNETSCPADCDP 93
TRBM HUMAN|P07204 ( 401) PHRCQMFCNQATACPADCDP 100
//

```

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Block PR00907G

```

ID    THRMBOMODULN; BLOCK
AC    PR00907G; distance from previous block=(35,35)
DE    Thrombomodulin signature
BL    adapted; width=27; seqs=3; 99.5%=1038; strength=1431
O35370      ( 454) CRNLPGSYECICGPDTALAGQISKDCD 80
TRBM MOUSE|P15306 ( 454) CRNFPGSYECICGPDTALAGQISKDCD 83
TRBM HUMAN|P07204 ( 455) CHNLPGTFCICGPDSALARHIGTDCD 100
//

```

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Block PR00907H

```

ID    THRMBOMODULN; BLOCK
AC    PR00907H; distance from previous block=(32,35)
DE    Thrombomodulin signature
BL    adapted; width=25; seqs=3; 99.5%=918; strength=1397
O35370      ( 516) HSGVLIGISIASLSLVVALLALLCH 94
TRBM MOUSE|P15306 ( 516) HSGVLIGISIASLSLVVALLALLCH 94
TRBM HUMAN|P07204 ( 514) HSGLLIGISIASLCLVVALLALLCH 100
//

```

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Block PR00907I

```

ID    THRMBOMODULN; BLOCK
AC    PR00907I; distance from previous block=(8,8)
DE    Thrombomodulin signature
BL    adapted; width=25; seqs=3; 99.5%=931; strength=1340
O35370      ( 549) RAELEYKCTSSAKEVVLQHVRTDRT 86
TRBM MOUSE|P15306 ( 549) RAELEYKCASSAKEVVLQHVRTDRT 84
TRBM HUMAN|P07204 ( 547) RAKMEYKCAAPSKEVVLQHVRTERT 100

```

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COBBLER sequence (region containing Blocks only)

To do a BLAST search, copy the cobbler sequence below then click on a BLAST link

[\[Blast Search\]](#) [\[Gap-Blast Search\]](#) [\[PSI-Blast Search\]](#)

COBBLER sequence:

```
>PR00907 035370|035370 from 222 to 577 with embedded consensus blocks
vcralpgtseGHWAREATGAWNCSVENGGCCEYMCNRS PNGPRCLCPggdlLQADGRSCAKPVTQSCNELCEHFCnnsdv
pgsyscmcetgyqlaadghrcevdvddckqgpnpcpqlcsntegGGFECHCYDGYELVDGECVEPLDPCFskcCEYQCQPV
NPTHYRCICAEGFAPlddpPHRCMFNETSCPADCDPspfcqcpegfildegstctdidecsqgecltnecCRNLPGS
YECICGPD TALAGQISKDCDipvledsedggsghepssnptvvsstvpssarpmhHSGVLIIGISIASLCLVVAL LALLCH
rkkqgtarRAELEYKCASSAKEVVLQHVRTDRTqkf
```

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Additional Links (separate browser window)

[InterPro IPR001491](#)
[PROSITE PS00022](#)
[MetaFam PR00907](#)

[\[Blocks home\]](#)